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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/456,306	12/08/1999	NICOLE DUSCH	PM-265182	6287

909 7590 11/03/2004

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EXAMINER	
STEADMAN, DAVID J	

ART UNIT	PAPER NUMBER
1652	

DATE MAILED: 11/03/2004

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	09/456,306	DUSCH ET AL.	
	Examiner	Art Unit	
	David J Steadman	1652	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *16 September 2004*.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *35-41 and 43-52* is/are pending in the application.

4a) Of the above claim(s) _____ is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *35-38,40,41 and 43-52* is/are rejected.

7)☒ Claim(s) *39* is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☒ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☒ All b)☐ Some * c)☐ None of:

1.☒ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☐ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08) Paper No(s)/Mail Date _____.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____.
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☒ Other: *Appendices A-D*.

DETAILED ACTION

Status of the Application

[1] Claims 35-41 and 43-52 are pending in the application.

[2] Applicants' amendment to the claims, filed September 16, 2004, is acknowledged. This listing of the claims replaces all prior versions and listings of the claims.

[3] Applicants' amendment to the specification, filed September 16, 2004, is acknowledged.

[4] Receipt of an amended abstract to the specification, filed September 16, 2004, is acknowledged.

[5] Receipt of a computer readable form of the sequence listing, a paper copy thereof, a statement of their sameness, and a statement that the paper copy of the sequence listing contains no new matter, all filed September 16, 2004, is acknowledged.

[6] Applicants' arguments filed on September 16, 2004 have been fully considered. Rejections and/or objections not reiterated from previous office actions are hereby withdrawn.

[7] The text of those sections of Title 35, U.S. Code not included in the instant action can be found in a prior Office action.

[8] The indicated allowability of claims 35 and 37-41 is withdrawn in view of the new rejections as set forth below.

Claim Objections

[9] Claim 37 is objected to under 37 CFR 1.75(c), as being of improper dependent form for failing to further limit the subject matter of a previous claim. Applicant is required to cancel the claim(s), or amend the claim(s) to place the claim(s) in proper dependent form, or rewrite the claim(s) in independent form. Claim 35 encompasses any nucleic acid that encodes SEQ ID NO:2, including all degenerate variants thereof. As such, claim 37 does not further limit claim 35.

Claim Rejections - 35 USC § 112, Second Paragraph

[10] Claim(s) 45-46 and 50-52 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

Claims 45 (claim 46 dependent therefrom) and 50 (claims 51-52 dependent therefrom) are confusing in that the claims recite "the nucleic acid molecule of claim 42," however, claim 42 has been canceled. It is suggested that applicants clarify the meaning of the claims. In the interest of advancing prosecution, the examiner has interpreted claims 45 and 50 as being dependent upon claim 44 instead of claim 42.

Claim Rejections - 35 USC § 112, First Paragraph

[11] Claims 36, 38, 40-41, and 50-52 are rejected under 35 U.S.C. 112, first paragraph, because the specification, while being enabling for a nucleic acid encoding SEQ ID NO:2, including SEQ ID NO:1, does not reasonably provide enablement for the

broad scope of claimed nucleic acids. The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention commensurate in scope with these claims.

It is the examiner's position that undue experimentation would be required for a skilled artisan to make and/or use the entire scope of polynucleotides of claims 36 (claims 38 and 40-41 dependent therefrom) and 50 (claims 51-52 dependent therefrom) for the reasons of record as set forth at item [9] of the Office action mailed June 16, 2004.

RESPONSE TO ARGUMENTS: Applicants argue the variants encompassed by the claims must retain the utility of the DNA sequence allegedly discovered by applicants. Applicants the specification enables a skilled artisan to make and use all variants encompassed within the scope of the claims using routine recombinant DNA techniques that are acknowledged by Example 14 of the Office's Revised Interim Written Description Guidelines Training Materials and pyruvate oxidase activity assays that were known in the art at the time of the invention. Applicants further argue the specification provides guidance as to the types of changes that are more likely to retain functionality. Applicants provide Attachments A and B as evidence. Applicants' argument is not found persuasive.

There is no dispute that recombinant DNA techniques for isolating and altering an encoding polynucleotide sequence and methods of assaying pyruvate oxidase enzymatic activity were known in the art at the time of the invention. It should be noted that, while the Office's Revised Interim Written Description Guidelines Training Materials

indicate that such techniques were known in the art, applicants are reminded that "the written description requirement is separate and distinct from the enablement requirement" (MPEP 2161). The fact that such techniques were known does not necessarily indicate an enabling disclosure for the scope of claimed polynucleotide variants. In this case, the specification is silent with regard to guidance for determining which of those nucleotides of SEQ ID NO:1 can be altered with an expectation of obtaining an encoded polypeptide having pyruvate oxidase activity. While it is acknowledged that the specification provides a general discussion of mutations (p. 10, lines 15-30), this disclosure fails to provide any specific guidance regarding altering the sequence of SEQ ID NO:1. The variants encompassed by claims 36 and 50 is vast, including any variant having an insertion, addition, deletion, or substitution and any combination thereof within the identity or hybridization limitation as recited in the claims. As the claims encompass any variant as described above and in view of the lack of guidance in the specification and prior art, at the time of the invention it was highly unpredictable as to which nucleotides of SEQ ID NO:1 could have been altered while encoding a polypeptide that maintains pyruvate oxidase activity as evidenced by state of the art as represented by Branden and Witkowski et al. (cited in a previous Office action), the teachings of which are undisputed by applicants. Because the claims encompass a vast number of variants, the specification provides no specific guidance regarding alteration of SEQ ID NO:1 with an expectation of obtaining the desired variant, there is a high level of unpredictability, and the experimentation required to

make all variants as broadly encompassed by the claims was not routine, undue experimentation is required to make all variants as encompassed by the claims.

Claim Rejections - 35 USC § 102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

A person shall be entitled to a patent unless –

(e) the invention was described in (1) an application for patent, published under section 122(b), by another filed in the United States before the invention by the applicant for patent or (2) a patent granted on an application for patent by another filed in the United States before the invention by the applicant for patent, except that an international application filed under the treaty defined in section 351(a) shall have the effects for purposes of this subsection of an application filed in the United States only if the international application designated the United States and was published under Article 21(2) of such treaty in the English language.

[12] Claim(s) 35-38, 40-41, and 43-52 are rejected under 35 U.S.C. 102(b) as being anticipated by Pompejus et al. (US Patent Application Publication 2004/0180408 A1). The date relied upon for applying Pompejus et al. as prior art is August 31, 1999. The claims (in relevant part) are drawn to nucleic acids encoding SEQ ID NO:2, variants thereof, vectors and host cells, and a fragment of SEQ ID NO:1.

Pompejus et al. teaches a nucleic acid, SEQ ID NO:85, encoding a polypeptide that is 100% identical to SEQ ID NO:2 of the instant application (see Appendix A) and teach fragments and complements of their nucleic acid (p. 11). Pompejus et al. teach a vector comprising their nucleic acid and a host cell comprising said vector (pp. 14-17). This anticipates claims 35-38, 40-41, and 43-52 as written.

[13] It should be noted that the polynucleotide of SEQ ID NO:1 of the instant application appears to be novel over Pompejus et al. While nucleotides 227 to 2086 of SEQ ID NO:1 are identical to the full length of SEQ ID NO:85 of Pompejus et al., nucleotides 1-226 of SEQ ID NO:1 are not disclosed by Pompejus et al. Thus, Pompejus et al. does not disclose the full length of SEQ ID NO:1 of the instant application. See Appendix B.

[14] It should also be noted that claim 39 has not been rejected as being anticipated or made obvious by Pompejus et al. According to the specification (see p. 18, middle), vector pCR2.1poxBint has a fragment of nucleotides 705 to 1579 of SEQ ID NO:1 (see Appendix C), encoding amino acids 127 to 417 of SEQ ID NO:2 (see Appendix D). The examiner can find no teaching in the prior art of record for a pCR2.1 vector having an insert of nucleotides 705 to 1579 of SEQ ID NO:1.

Conclusion

[15] Status of the claims:

- Claims 35-41 and 43-52 are pending.
- Claims 35-38, 40-41, and 43-52 are rejected.
- Claim 39 is objected to as being dependent upon a rejected base claim, but would be allowable if rewritten in independent form including all of the limitations of the base claim and any intervening claims.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to David Steadman, whose telephone number is (571) 272-0942. The Examiner can normally be reached Monday-Friday from 7:30 am to 4:00 pm. If attempts to reach the Examiner by telephone are unsuccessful, the Examiner's supervisor, Ponnathapura Achutamurthy, can be reached at (571) 272-0928. Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to the Art Unit receptionist whose telephone number is (703) 308-0196.

10-28-04

David J. Steadman, Ph.D.
Primary Examiner
Art Unit 1652

APPENDIX A

RESULT 1
us-10-781-014-85

Alignment Scores:

Pred. No.:	0	Length:	1860
Score:	2985.00	Matches:	579
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	1	Gaps:	0

US-09-456-306-2 (1-579) x us-10-781-014-85 (1-1860)

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Qy          1 MetAlaHisSerTyrAlaGluGlnLeuIleAspThrLeuGluAlaGlnGlyValLysArg 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        101 ATGGCACACAGCTACGCAGAACAATTAATTGACACTTTGGAAGCTCAAGGTGTGAAGCGA 160

Qy         21 IleTyrGlyLeuValGlyAspSerLeuAsnProIleValAspAlaValArgGlnSerAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        161 ATTTATGGTTTGGTGGGTGACAGCCTTAATCCGATCGTGGATGCTGTCCGCCAATCAGAT 220

Qy         41 IleGluTrpValHisValArgAsnGluGluAlaAlaAlaPheAlaAlaGlyAlaGluSer 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        221 ATTGAGTGGGTGCACGTTCGAAATGAGGAAGCGGCGGCGTTTGCAGCCGGTGCGGAATCG 280

Qy         61 LeuIleThrGlyGluLeuAlaValCysAlaAlaSerCysGlyProGlyAsnThrHisLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        281 TTGATCACTGGGGAGCTGGCAGTATGTGCTGCTTCTTGTGGTCCTGGAAACACACACCTG 340

Qy         81 IleGlnGlyLeuTyrAspSerHisArgAsnGlyAlaLysValLeuAlaIleAlaSerHis 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        341 ATTCAGGGTCTTTATGATTCGCATCGAAATGGTGCGAAGGTGTTGGCCATCGCTAGCCAT 400

Qy        101 IleProSerAlaGlnIleGlySerThrPhePheGlnGluThrHisProGluIleLeuPhe 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        401 ATTCCGAGTGCCCAGATTGGTTCGACGTTCTTCCAGGAAACGCATCCGGAGATTTTGTTT 460

Qy        121 LysGluCysSerGlyTyrCysGluMetValAsnGlyGlyGluGlnGlyGluArgIleLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        461 AAGGAATGCTCTGGTTACTGCGAGATGGTGAATGGTGGTGAGCAGGGTGAACGCATTTTG 520

Qy        141 HisHisAlaIleGlnSerThrMetAlaGlyLysGlyValSerValValValIleProGly 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        521 CATCACGCGATTCAGTCCACCATGGCGGGTAAAGGTGTGTCGGTGGTAGTGATTCCTGGT 580

Qy        161 AspIleAlaLysGluAspAlaGlyAspGlyThrTyrSerAsnSerThrIleSerSerGly 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        581 GATATCGCTAAGGAAGACGCAGGTGACGGTACTTATTCCAATTCCACTATTTCTTCTGGC 640

Qy        181 ThrProValValPheProAspProThrGluAlaAlaAlaLeuValGluAlaIleAsnAsn 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        641 ACTCCTGTGGTGTTCCCGGATCCTACTGAGGCTGCAGCGCTGGTGGAGGCGATTAACAAC 700

Qy        201 AlaLysSerValThrLeuPheCysGlyAlaGlyValLysAsnAlaArgAlaGlnValLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        701 GCTAAGTCTGTCACTTTGTTCTGCGGTGCGGGCGTGAAGAATGCTCGCGCGCAGGTGTTG 760

Qy        221 GluLeuAlaGluLysIleLysSerProIleGlyHisAlaLeuGlyGlyLysGlnTyrIle 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        761 GAGTTGGCGGAGAAGATTAAATCACCGATCGGGCATGCGCTGGGTGGTAAGCAGTACATC 820

Qy        241 GlnHisGluAsnProPheGluValGlyMetSerGlyLeuLeuGlyTyrGlyAlaCysVal 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        821 CAGCATGAGAATCCGTTTGAGGTCGGCATGTCTGGCCTGCTTGGTTACGGCGCCTGCGTG 880

Qy        261 AspAlaSerAsnGluAlaAspLeuLeuIleLeuLeuGlyThrAspProTyrSerAsp 280
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Db        881 GATGCGTCCAATGAGGCGGATCTGCTGATTCTATTGGGTACGGATTTCCCTTATTCTGAT 940

Qy        281 PheLeuProLysAspAsnValAlaGlnValAspIleAsnGlyAlaHisIleGlyArgArg 300

Db        941 TTCCTTCCTAAAGACAACGTTGCCCAGGTGGATATCAACGGTGCGCACATTGGTCGACGT 1000

Qy        301 ThrThrValLysTyrProValThrGlyAspValAlaAlaThrIleGluAsnIleLeuPro 320

Db       1001 ACCACGGTGAAGTATCCGGTGACCGGTGATGTTGCTGCAACAATCGAAAATATTTTGCCT 1060

Qy        321 HisValLysGluLysThrAspArgSerPheLeuAspArgMetLeuLysAlaHisGluArg 340

Db       1061 CATGTGAAGGAAAAAACAGATCGTTCCTTCCTTGATCGGATGCTCAAGGCACACGAGCGT 1120

Qy        341 LysLeuSerSerValValGluThrTyrThrHisAsnValGluLysHisValProIleHis 360

Db       1121 AAGTTGAGCTCGGTGGTAGAGACGTACACACATAACGTCGAGAAGCATGTGCCTATTCAC 1180

Qy        361 ProGluTyrValAlaSerIleLeuAsnGluLeuAlaAspLysAspAlaValPheThrVal 380

Db       1181 CCTGAATACGTTGCCTCTATTTTGAACGAGCTGGCGGATAAGGATGCGGTGTTTACTGTG 1240

Qy        381 AspThrGlyMetCysAsnValTrpHisAlaArgTyrIleGluAsnProGluGlyThrArg 400

Db       1241 GATACCGGCATGTGCAATGTGTGGCATGCGAGGTACATCGAGAATCCGGAGGGAACGCGC 1300

Qy        401 AspPheValGlySerPheArgHisGlyThrMetAlaAsnAlaLeuProHisAlaIleGly 420

Db       1301 GACTTTGTGGGTTCATTCCGCCACGGCACGATGGCTAATGCGTTGCCTCATGCGATTGGT 1360

Qy        421 AlaGlnSerValAspArgAsnArgGlnValIleAlaMetCysGlyAspGlyGlyLeuGly 440

Db       1361 GCGCAAAGTGTTGATCGAAACCGCCAGGTGATCGCGATGTGTGGCGATGGTGGTTTGGGC 1420

Qy        441 MetLeuLeuGlyGluLeuLeuThrValLysLeuHisGlnLeuProLeuLysAlaValVal 460

Db       1421 ATGCTGCTGGGTGAGCTTCTGACCGTTAAGCTGCACCAACTTCCGCTGAAGGCTGTGGTG 1480

Qy        461 PheAsnAsnSerSerLeuGlyMetValLysLeuGluMetLeuValGluGlyGlnProGlu 480

Db       1481 TTTAACAACAGTTCTTTGGGCATGGTGAAGTTGGAGATGCTCGTGGAGGGACAGCCAGAA 1540

Qy        481 PheGlyThrAspHisGluGluValAsnPheAlaGluIleAlaAlaAlaAlaGlyIleLys 500

Db       1541 TTTGGTACTGACCATGAGGAAGTGAATTTCGCAGAGATTGCGGCGGCTGCGGGTATCAAA 1600

Qy        501 SerValArgIleThrAspProLysLysValArgGluGlnLeuAlaGluAlaLeuAlaTyr 520

Db       1601 TCGGTACGCATCACCGATCCGAAGAAAGTTCGCGAGCAGCTAGCTGAGGCATTGGCATAT 1660

Qy        521 ProGlyProValLeuIleAspIleValThrAspProAsnAlaLeuSerIleProProThr 540

Db       1661 CCTGGACCTGTACTGATCGATATCGTCACGGATCCTAATGCGCTGTCGATCCCACCAACC 1720

Qy        541 IleThrTrpGluGlnValMetGlyPheSerLysAlaAlaThrArgThrValPheGlyGly 560

Db       1721 ATCACGTGGGAACAGGTCATGGGATTCAGCAAGGCGGCCACCCGAACCGTCTTTGGTGGA 1780

Qy        561 GlyValGlyAlaMetIleAspLeuAlaArgSerAsnIleArgAsnIleProThrPro 579

Db       1781 GGAGTAGGAGCGATGATCGATCTGGCCCGTTCGAACATAAGGAATATTCCTACTCCA 1837
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APPENDIX B

RESULT 1
us-10-781-014-85

Query Match 86.1%; Score 1860; DB 1; Length 1860;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1860; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       227 CTGGCAGGCGGGCGAAGCGTGGCAACAACTGGAATTTAAGAGCACAATTGAAGTCGCACC 286
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1 CTGGCAGGCGGGCGAAGCGTGGCAACAACTGGAATTTAAGAGCACAATTGAAGTCGCACC 60

Qy       287 AAGTTAGGCAACACAATAGCCATAACGTTGAGGAGTTCAGATGGCACACAGCTACGCAGA 346
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 AAGTTAGGCAACACAATAGCCATAACGTTGAGGAGTTCAGATGGCACACAGCTACGCAGA 120

Qy       347 ACAATTAATTGACACTTTGGAAGCTCAAGGTGTGAAGCGAATTTATGGTTTGGTGGGTGA 406
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 ACAATTAATTGACACTTTGGAAGCTCAAGGTGTGAAGCGAATTTATGGTTTGGTGGGTGA 180

Qy       407 CAGCCTTAATCCGATCGTGGATGCTGTCCGCCAATCAGATATTGAGTGGGTGCACGTTCG 466
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 CAGCCTTAATCCGATCGTGGATGCTGTCCGCCAATCAGATATTGAGTGGGTGCACGTTCG 240

Qy       467 AAATGAGGAAGCGGCGGCGTTTGCAGCCGGTGCGGAATCGTTGATCACTGGGGAGCTGGC 526
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       241 AAATGAGGAAGCGGCGGCGTTTGCAGCCGGTGCGGAATCGTTGATCACTGGGGAGCTGGC 300

Qy       527 AGTATGTGCTGCTTCTTGTGGTCCTGGAAACACACACCTGATTCAGGGTCTTTATGATTC 586
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       301 AGTATGTGCTGCTTCTTGTGGTCCTGGAAACACACACCTGATTCAGGGTCTTTATGATTC 360

Qy       587 GCATCGAAATGGTGCGAAGGTGTTGGCCATCGCTAGCCATATTCCGAGTGCCCAGATTGG 646
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       361 GCATCGAAATGGTGCGAAGGTGTTGGCCATCGCTAGCCATATTCCGAGTGCCCAGATTGG 420

Qy       647 TTCGACGTTCTTCCAGGAAACGCATCCGGAGATTTTGTTTAAGGAATGCTCTGGTTACTG 706
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       421 TTCGACGTTCTTCCAGGAAACGCATCCGGAGATTTTGTTTAAGGAATGCTCTGGTTACTG 480

Qy       707 CGAGATGGTGAATGGTGGTGAGCAGGGTGAACGCATTTTGCATCACGCGATTCAGTCCAC 766
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       481 CGAGATGGTGAATGGTGGTGAGCAGGGTGAACGCATTTTGCATCACGCGATTCAGTCCAC 540

Qy       767 CATGGCGGGTAAAGGTGTGTCGGTGGTAGTGATTCCTGGTGATATCGCTAAGGAAGACGC 826
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       541 CATGGCGGGTAAAGGTGTGTCGGTGGTAGTGATTCCTGGTGATATCGCTAAGGAAGACGC 600

Qy       827 AGGTGACGGTACTTATTCCAATTCCACTATTTCTTCTGGCACTCCTGTGGTGTTCCCGGA 886
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       601 AGGTGACGGTACTTATTCCAATTCCACTATTTCTTCTGGCACTCCTGTGGTGTTCCCGGA 660

Qy       887 TCCTACTGAGGCTGCAGCGCTGGTGGAGGCGATTAACAACGCTAAGTCTGTCACTTTGTT 946
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       661 TCCTACTGAGGCTGCAGCGCTGGTGGAGGCGATTAACAACGCTAAGTCTGTCACTTTGTT 720

Qy       947 CTGCGGTGCGGGCGTGAAGAATGCTCGCGCGCAGGTGTTGGAGTTGGCGGAGAAGATTAA 1006
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       721 CTGCGGTGCGGGCGTGAAGAATGCTCGCGCGCAGGTGTTGGAGTTGGCGGAGAAGATTAA 780

Qy      1007 ATCACCGATCGGGCATGCGCTGGGTGGTAAGCAGTACATCCAGCATGAGAATCCGTTTGA 1066
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       781 ATCACCGATCGGGCATGCGCTGGGTGGTAAGCAGTACATCCAGCATGAGAATCCGTTTGA 840

Qy      1067 GGTCGGCATGTCTGGCCTGCTTGGTTACGGCGCCTGCGTGGATGCGTCCAATGAGGCGGA 1126
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       841 GGTCGGCATGTCTGGCCTGCTTGGTTACGGCGCCTGCGTGGATGCGTCCAATGAGGCGGA 900
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Qy       1127 TCTGCTGATTCTATTGGGTACGGATTTCCCTTATTCTGATTTCCTTCCTAAAGACAACGT 1186
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TCTGCTGATTCTATTGGGTACGGATTTCCCTTATTCTGATTTCCTTCCTAAAGACAACGT 960

Qy       1187 TGCCCAGGTGGATATCAACGGTGCGCACATTGGTCGACGTACCACGGTGAAGTATCCGGT 1246
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TGCCCAGGTGGATATCAACGGTGCGCACATTGGTCGACGTACCACGGTGAAGTATCCGGT 1020

Qy       1247 GACCGGTGATGTTGCTGCAACAATCGAAAATATTTTGCCTCATGTGAAGGAAAAAACAGA 1306
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GACCGGTGATGTTGCTGCAACAATCGAAAATATTTTGCCTCATGTGAAGGAAAAAACAGA 1080

Qy       1307 TCGTTCCTTCCTTGATCGGATGCTCAAGGCACACGAGCGTAAGTTGAGCTCGGTGGTAGA 1366
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TCGTTCCTTCCTTGATCGGATGCTCAAGGCACACGAGCGTAAGTTGAGCTCGGTGGTAGA 1140

Qy       1367 GACGTACACACATAACGTCGAGAAGCATGTGCCTATTCACCCTGAATACGTTGCCTCTAT 1426
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GACGTACACACATAACGTCGAGAAGCATGTGCCTATTCACCCTGAATACGTTGCCTCTAT 1200

Qy       1427 TTTGAACGAGCTGGCGGATAAGGATGCGGTGTTTACTGTGGATACCGGCATGTGCAATGT 1486
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 TTTGAACGAGCTGGCGGATAAGGATGCGGTGTTTACTGTGGATACCGGCATGTGCAATGT 1260

Qy       1487 GTGGCATGCGAGGTACATCGAGAATCCGGAGGGAACGCGCGACTTTGTGGGTTCATTCCG 1546
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GTGGCATGCGAGGTACATCGAGAATCCGGAGGGAACGCGCGACTTTGTGGGTTCATTCCG 1320

Qy       1547 CCACGGCACGATGGCTAATGCGTTGCCTCATGCGATTGGTGCGCAAAGTGTTGATCGAAA 1606
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 CCACGGCACGATGGCTAATGCGTTGCCTCATGCGATTGGTGCGCAAAGTGTTGATCGAAA 1380

Qy       1607 CCGCCAGGTGATCGCGATGTGTGGCGATGGTGGTTTGGGCATGCTGCTGGGTGAGCTTCT 1666
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CCGCCAGGTGATCGCGATGTGTGGCGATGGTGGTTTGGGCATGCTGCTGGGTGAGCTTCT 1440

Qy       1667 GACCGTTAAGCTGCACCAACTTCCGCTGAAGGCTGTGGTGTTTAACAACAGTTCTTTGGG 1726
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 GACCGTTAAGCTGCACCAACTTCCGCTGAAGGCTGTGGTGTTTAACAACAGTTCTTTGGG 1500

Qy       1727 CATGGTGAAGTTGGAGATGCTCGTGGAGGGACAGCCAGAATTTGGTACTGACCATGAGGA 1786
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 CATGGTGAAGTTGGAGATGCTCGTGGAGGGACAGCCAGAATTTGGTACTGACCATGAGGA 1560

Qy       1787 AGTGAATTTCGCAGAGATTGCGGCGGCTGCGGGTATCAAATCGGTACGCATCACCGATCC 1846
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 AGTGAATTTCGCAGAGATTGCGGCGGCTGCGGGTATCAAATCGGTACGCATCACCGATCC 1620

Qy       1847 GAAGAAAGTTCGCGAGCAGCTAGCTGAGGCATTGGCATATCCTGGACCTGTACTGATCGA 1906
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 GAAGAAAGTTCGCGAGCAGCTAGCTGAGGCATTGGCATATCCTGGACCTGTACTGATCGA 1680

Qy       1907 TATCGTCACGGATCCTAATGCGCTGTCGATCCCACCAACCATCACGTGGGAACAGGTCAT 1966
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 TATCGTCACGGATCCTAATGCGCTGTCGATCCCACCAACCATCACGTGGGAACAGGTCAT 1740

Qy       1967 GGGATTCAGCAAGGCGGCCACCCGAACCGTCTTTGGTGGAGGAGTAGGAGCGATGATCGA 2026
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 GGGATTCAGCAAGGCGGCCACCCGAACCGTCTTTGGTGGAGGAGTAGGAGCGATGATCGA 1800

Qy       2027 TCTGGCCCGTTCGAACATAAGGAATATTCCTACTCCATGATGATTGATACACCTGCTGTT 2086
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 TCTGGCCCGTTCGAACATAAGGAATATTCCTACTCCATGATGATTGATACACCTGCTGTT 1860
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APPENDIX C

RESULT 1
us-09-456-306-1

Query Match 100.0%; Score 875; DB 1; Length 2160;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 875; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 TGCGAGATGGTGAATGGTGGTGAGCAGGGTGAACGCATTTTGCATCACGCGATTCAGTCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        705 TGCGAGATGGTGAATGGTGGTGAGCAGGGTGAACGCATTTTGCATCACGCGATTCAGTCC 764

Qy         61 ACCATGGCGGGTAAAGGTGTGTCGGTGGTAGTGATTCCTGGTGATATCGCTAAGGAAGAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        765 ACCATGGCGGGTAAAGGTGTGTCGGTGGTAGTGATTCCTGGTGATATCGCTAAGGAAGAC 824

Qy        121 GCAGGTGACGGTACTTATTCCAATTCCACTATTTCTTCTGGCACTCCTGTGGTGTTCCCG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        825 GCAGGTGACGGTACTTATTCCAATTCCACTATTTCTTCTGGCACTCCTGTGGTGTTCCCG 884

Qy        181 GATCCTACTGAGGCTGCAGCGCTGGTGGAGGCGATTAACAACGCTAAGTCTGTCACTTTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        885 GATCCTACTGAGGCTGCAGCGCTGGTGGAGGCGATTAACAACGCTAAGTCTGTCACTTTG 944

Qy        241 TTCTGCGGTGCGGGCGTGAAGAATGCTCGCGCGCAGGTGTTGGAGTTGGCGGAGAAGATT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        945 TTCTGCGGTGCGGGCGTGAAGAATGCTCGCGCGCAGGTGTTGGAGTTGGCGGAGAAGATT 1004

Qy        301 AAATCACCGATCGGGCATGCGCTGGGTGGTAAGCAGTACATCCAGCATGAGAATCCGTTT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1005 AAATCACCGATCGGGCATGCGCTGGGTGGTAAGCAGTACATCCAGCATGAGAATCCGTTT 1064

Qy        361 GAGGTCGGCATGTCTGGCCTGCTTGGTTACGGCGCCTGCGTGGATGCGTCCAATGAGGCG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1065 GAGGTCGGCATGTCTGGCCTGCTTGGTTACGGCGCCTGCGTGGATGCGTCCAATGAGGCG 1124

Qy        421 GATCTGCTGATTCTATTGGGTACGGATTTCCCTTATTCTGATTTCCTTCCTAAAGACAAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1125 GATCTGCTGATTCTATTGGGTACGGATTTCCCTTATTCTGATTTCCTTCCTAAAGACAAC 1184

Qy        481 GTTGCCCAGGTGGATATCAACGGTGCGCACATTGGTCGACGTACCACGGTGAAGTATCCG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1185 GTTGCCCAGGTGGATATCAACGGTGCGCACATTGGTCGACGTACCACGGTGAAGTATCCG 1244

Qy        541 GTGACCGGTGATGTTGCTGCAACAATCGAAAATATTTTGCCTCATGTGAAGGAAAAAACA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1245 GTGACCGGTGATGTTGCTGCAACAATCGAAAATATTTTGCCTCATGTGAAGGAAAAAACA 1304

Qy        601 GATCGTTCCTTCCTTGATCGGATGCTCAAGGCACACGAGCGTAAGTTGAGCTCGGTGGTA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1305 GATCGTTCCTTCCTTGATCGGATGCTCAAGGCACACGAGCGTAAGTTGAGCTCGGTGGTA 1364

Qy        661 GAGACGTACACACATAACGTCGAGAAGCATGTGCCTATTCACCCTGAATACGTTGCCTCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1365 GAGACGTACACACATAACGTCGAGAAGCATGTGCCTATTCACCCTGAATACGTTGCCTCT 1424

Qy        721 ATTTTGAACGAGCTGGCGGATAAGGATGCGGTGTTTACTGTGGATACCGGCATGTGCAAT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1425 ATTTTGAACGAGCTGGCGGATAAGGATGCGGTGTTTACTGTGGATACCGGCATGTGCAAT 1484

Qy        781 GTGTGGCATGCGAGGTACATCGAGAATCCGGAGGGAACGCGCGACTTTGTGGGTTCATTC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1485 GTGTGGCATGCGAGGTACATCGAGAATCCGGAGGGAACGCGCGACTTTGTGGGTTCATTC 1544

Qy        841 CGCCACGGCACGATGGCTAATGCGTTGCCTCATGC 875
              ||||||||||||||||||||||||||||||||||
Db       1545 CGCCACGGCACGATGGCTAATGCGTTGCCTCATGC 1579
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APPENDIX D

RESULT 1
us-09-456-306-3

Alignment Scores:

Pred. No.:	0	Length:	875
Score:	1518.00	Matches:	291
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	50.85%	Indels:	0
DB:	1	Gaps:	0

us-09-456-306-2 (1-579) x us-09-456-306-3 (1-875)

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Qy        127 CysGluMetValAsnGlyGlyGluGlnGlyGluArgIleLeuHisHisAlaIleGlnSer 146
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TGCGAGATGGTGAATGGTGGTGAGCAGGGTGAACGCATTTTGCATCACGCGATTCAGTCC 60

Qy        147 ThrMetAlaGlyLysGlyValSerValValValIleProGlyAspIleAlaLysGluAsp 166
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACCATGGCGGGTAAAGGTGTGTCGGTGGTAGTGATTCCTGGTGATATCGCTAAGGAAGAC 120

Qy        167 AlaGlyAspGlyThrTyrSerAsnSerThrIleSerSerGlyThrProValValPhePro 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCAGGTGACGGTACTTATTCCAATTCCACTATTTCTTCTGGCACTCCTGTGGTGTTCCCG 180

Qy        187 AspProThrGluAlaAlaAlaLeuValGluAlaIleAsnAsnAlaLysSerValThrLeu 206
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GATCCTACTGAGGCTGCAGCGCTGGTGGAGGCGATTAACAACGCTAAGTCTGTCACTTTG 240

Qy        207 PheCysGlyAlaGlyValLysAsnAlaArgAlaGlnValLeuGluLeuAlaGluLysIle 226
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TTCTGCGGTGCGGGCGTGAAGAATGCTCGCGCGCAGGTGTTGGAGTTGGCGGAGAAGATT 300

Qy        227 LysSerProIleGlyHisAlaLeuGlyGlyLysGlnTyrIleGlnHisGluAsnProPhe 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AAATCACCGATCGGGCATGCGCTGGGTGGTAAGCAGTACATCCAGCATGAGAATCCGTTT 360

Qy        247 GluValGlyMetSerGlyLeuLeuGlyTyrGlyAlaCysValAspAlaSerAsnGluAla 266
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GAGGTCGGCATGTCTGGCCTGCTTGGTTACGGCGCCTGCGTGGATGCGTCCAATGAGGCG 420

Qy        267 AspLeuLeuIleLeuLeuGlyThrAspPheProTyrSerAspPheLeuProLysAspAsn 286
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GATCTGCTGATTCTATTGGGTACGGATTTCCCTTATTCTGATTTCCTTCCTAAAGACAAC 480

Qy        287 ValAlaGlnValAspIleAsnGlyAlaHisIleGlyArgArgThrThrValLysTyrPro 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTTGCCCAGGTGGATATCAACGGTGCGCACATTGGTCGACGTACCACGGTGAAGTATCCG 540

Qy        307 ValThrGlyAspValAlaAlaThrIleGluAsnIleLeuProHisValLysGluLysThr 326
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTGACCGGTGATGTTGCTGCAACAATCGAAAATATTTTGCCTCATGTGAAGGAAAAAACA 600

Qy        327 AspArgSerPheLeuAspArgMetLeuLysAlaHisGluArgLysLeuSerSerValVal 346
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GATCGTTCCTTCCTTGATCGGATGCTCAAGGCACACGAGCGTAAGTTGAGCTCGGTGGTA 660

Qy        347 GluThrTyrThrHisAsnValGluLysHisValProIleHisProGluTyrValAlaSer 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAGACGTACACACATAACGTCGAGAAGCATGTGCCTATTCACCCTGAATACGTTGCCTCT 720

Qy        367 IleLeuAsnGluLeuAlaAspLysAspAlaValPheThrValAspThrGlyMetCysAsn 386
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATTTTGAACGAGCTGGCGGATAAGGATGCGGTGTTTACTGTGGATACCGGCATGTGCAAT 780

Qy        387 ValTrpHisAlaArgTyrIleGluAsnProGluGlyThrArgAspPheValGlySerPhe 406
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GTGTGGCATGCGAGGTACATCGAGAATCCGGAGGGAACGCGCGACTTTGTGGGTTCATTC 840

Qy        407 ArgHisGlyThrMetAlaAsnAlaLeuProHis 417
                ||||||||||||||||||||||||||||||||
Db        841 CGCCACGGCACGATGGCTAATGCGTTGCCTCAT 873
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